AMENDMENTS TO THE CLAIMS:

This listing of claims will replace all prior versions and listing of the claims in the application:

LISTING OF THE CLAIMS:

Claim 1. (currently amended) A method for identifying a plurality of different types of infectious particles in a sample containing a plurality of different types of infectious particles comprising;

separating an infectious particle containing fraction from the sample,

extracting at least two nucleic acids from the fraction, wherein one of the nucleic acids is from a different type of infectious particle than another one of the nucleic acids,

sequencing at least a portion of each one of the at least two nucleic acids ~~or a complementary sequence thereof~~, to obtain a sequenced portion of each one of the at least two nucleic acids; or, sequencing at least a portion complementary thereto from which one may deduce a nucleotide sequence of the sequenced portion of each one of the at least two nucleic acids, and

determining the identity of the plurality of different types of infectious particles from the ~~sequence~~ sequenced portions or by overlapping sequences derived from the sequenced portions of the at least two ~~plural~~ nucleic acids.

Claim 2. (original) The method of claim 1 wherein the sample is a mixture of biological samples from plural individuals.

Claim 3. (original) The method of claim 1 further comprising comparing the sequence of the nucleic acids to a database of known sequences.

Claim 4. (original) The method of claim 3 wherein a new infectious particle is detected.

Claim 5. (original) The method of claim 4 wherein a known infectious particle is simultaneously detected.

Claim 6. (original) The method of claim 4 wherein plural new infectious particles are simultaneously detected.

Claim 7. (original) The method of claim 1 wherein the infectious particle is not cultured.

Claim 8. (original) The method of claim 1 wherein the nucleic acids are amplified in copy number between extracting and sequencing.

Claim 9. (original) The method of claim 1 wherein said fraction is separated by centrifugation.

Claim 10. (original) The method of claim 9 wherein the infectious particles band at a density between 1.05 and 1.3 gm/ml and exhibit sedimentation coefficients between 80 and 1,500 S.

Claim 11. (original) The method of claim 1 wherein said fraction is separated by filtration and a retentate is recovered.

Claim 12. (original) The method of claim 1 wherein said at least one nucleic acid is RNA and further comprising synthesizing a DNA complementary to said RNA.

Claim 13. (original) The method of claim 3 wherein the database contains nucleic acid sequences from known infectious particles or the sequences of the species from which the biological sample is obtained.

Claim 14. (original) The method of claim 1 wherein said nucleic acids are cleaved such that overlapping fragments are formed.

Claim 15. (canceled).

Claim 16. (original) The method of claim 1 wherein the sample is an aliquot from a composition intended for contacting a living organism.

Claims 17-58. (canceled).

Claim 59. (currently amended) The method of ~~claims~~ claim 1 ~~, 21, 29, 38, 47, or 49~~ wherein the method is performed in a containment system.

Claims 60-62. (canceled).

Claim 63. (previously presented) The method of claim 2 wherein the individuals are humans.

Claim 64. (currently amended) The method of claim 9 wherein the centrifugation is performed in a density gradient and wherein the sample is not cultured.

Claim 65. (currently amended) The method of claim 13 wherein the database contains sequences from different unrelated known infectious particles from different families of infectious particles.

Claim 66. (previously presented) The method of claim 1 wherein the samples are not suspected of containing a specific infectious particle.

Claim 67. (previously presented) The method of claim 1 wherein the sequences include at least part of a non-coding sequence of the infectious particle.

Claim 68. (previously presented) The method of claim 1 wherein the sequencing is performed by hybridization to an immobilized oligonucleotide microarray.